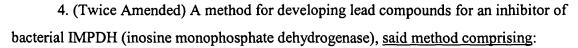
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- [a.](a) obtaining a crystal of bacterial IMPDH;
- [b.](b) recording x-ray diffraction data from said crystal;
- [c.](c) using said diffraction data to generate an electron density map consistent with <u>a</u> [the] model for the molecular structure of <u>a</u> binding pocket of IMPDH; and
- [d.](d) developing lead compounds for an inhibitor of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.
- 6. (Twice Amended) A crystalline molecule or molecular complex comprising [all or any parts] of a binding pocket wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.
- 7. (Twice Amended) A crystalline IMPDH molecule <u>defined by structural coordinates for IMPDH amino acids</u> [comprising coordinates] from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.

REMARKS

I. Status of the Claims

Applicant thanks Examiner Marschel for allowing claims 3 and 4, and potentially allowing claim 2 with a dependency amendment.

However, applicant requests clarification of the status of some other claims. The Interview Summary form only says claims 1 - 7 were discussed. The Advisory Action lists 1 - 8. Our records show claims 1 - 8 are pending.

We note that the amendments of February 13 and May 6, 2002 were not entered. Applicant had already cancelled claim 5 in the amendment mailed May 6, 2002, but claims 1 - 4 and 6 - 8 were still pending. Applicant now cancels claims 1 and 8 and again cancels claim 5, reserving the right to prosecute them in a continuing application.



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WE CLAIM:

- 2. The crystal of claim 3 further characterized by ability to provide x-ray diffraction patterns useful to define molecular structures for bacterial IMPDH enzymes.
- 3. A crystal of bacterial IMPDH (inosine monophosphate dehydrogenase) isolated from a bacterial preparation wherein the bacterial preparation is a pure culture of *Streptococcus pyogenes*.
- 4. A method for developing lead compounds for an inhibitor of bacterial IMPDH (inosine monophosphate dehydrogenase), said method comprising:
 - (a) obtaining a crystal of bacterial IMPDH;
 - (b) recording x-ray diffraction data from said crystal;
 - using said diffraction data to generate an electron density map consistent with a model for the molecular structure of a binding pocket of IMPDH; and
 - (d) developing lead compounds for an inhibitor of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.
- 6. A crystalline molecule or molecular complex comprising a binding pocket wherever said binding pocket is defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.
- 7. A crystalline IMPDH molecule defined by structural coordinates for IMPDH amino acids from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.



